#6

```
  1 CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC
    GGGTGCGCAG GCGTATTTAG TCGTGCGCCG GCCTCTTGGG GCGTTAGAGA CGCGGGTGTT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG

101 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGAACAACG GGGACAGAAC GCCCCGGCCG CTTCGGGGGC CCGGAAAAGG CACGGCCCAG
    GGTGCCCGGA CTCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTTGC CCCTGTCTTG CGGGGCCGGC GAAGCCCCCG GGCCTTTTCC GTGCCGGGTC
  1                                          M etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly

201 GACCCAGGGA GGCGCGGGGA GCCAGGCCTG GGCTCCGGGT CCCCAAGACC CTTGTGCTCG TTGTCGCCGC GGTCCTGCTG TTGGTCTCAG CTGAGTCTGC
    CTGGGTCCCT CCGCGCCCCT CGGTCCGGAC CCGAGGCCCA GGGGTTCTGG GAACACGAGC AACAGCGGCG CCAGGACGAC AACCAGAGTC GACTCAGACG
 22   ProArgGl uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSerA laGluSerAla

301 TCTGATCACC CAACAAGACC TAGCTCCCCA GCAGAGAGCG GCCCCACAAC AAAAGAGGTC CAGCCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC
    AGACTAGTGG GTTGTTCTGG ATCGAGGGGT CGTCTCTCGC CGGGGTGTTG TTTTCTCCAG GTCGGGGAGT CTCCCTAACA CAGGTGGACC TGTGGTATAG
 55  LeuIleThr GlnGlnAspL euAlaProGl nGlnArgAla AlaProGlnG lnLysArgSe rSerProSer GluGlyLeuC ysProProGl yHisHisIle

401 TCAGAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTGTGATT
    AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CGCGACGTGG TCCACACTAA
 88 SerGluAspG lyArgAspCy sIleSerCys LysTyrGlyG lnAspTyrSe rThrHisTrp AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer

501 CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGCGAAG AAGGCACCTT CCGGGAAGAA GATTCTCCTG AGATGTGCCG
    GTCCACTTCA CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTCACACA GTCACGCTTC TTCCGTGGAA GGCCCTTCTT CTAAGAGGAC TCTACACGGC
122   GlyGluVa lGluLeuSer ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg

601 GAAGTGCCGC ACAGGGTGTC CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCCTGGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA
    CTTCACGGCG TGTCCCACAG GGTCTCCCTA CCAGTTCCAG CCACTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT
155  LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerGl yIleIleIle

701 GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGCTGTGT TTGTTTGCAA GTCTTTACTG TGGAAGAAAG TCCTTCCTTA CCTGAAAGGC ATCTGCTCAG
    CCTCAGTGTC AACGTCGGCA TCAGAACTAA CACCGACACA AACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC
188 GlyValThrV alAlaAlaVa lValLeuIle ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly IleCysSerGly
```

FIG._1A

```
801  GTGGTGGTGG GGACCCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCCTCAA TGAGATCGTG AGTATCTTGC AGCCCACCCA
     CACCACCACC CCTGGGACTC GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT
222    GlyGlyGl yAspProGlu ArgValAspA rgSerSerGl nArgProGly AlaGluAspA snValLeuAs nGluIleVal SerIleLeuG lnProThrGln

901  GGTCCCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA
     CCAGGGACTC GTCCTTTACC TTCAGGTCCT CGGTCGTCTC GGTTGTCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT
255   ValProGlu GlnGluMetG luValGlnGl uProAlaGlu ProThrGlyV alAsnMetLe uSerProGly GluSerGluH isLeuLeuGl uProAlaGlu

1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGCTTCGA TGACTTTGCA GACTTGGTGC
     CGACTTTCCA GAGTCTCCTC CTCCGACGAC CAAGGTCGTT TACTTCCACT AGGGTGACTC TGAGACTCTG TCACGAAGCT ACTGAAACGT CTGAACCACG
288  AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG lnCysPheAs pAspPheAla AspLeuValPro

1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGCG GGCCACAGGG ACACCTTGTA
     GGAAACTGAG GACCCTCGGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTTCC ACCGATTTCG ACTCCGTCGC CCGGTGTCCC TGTGGAACAT
322    PheAspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluIleLysV alAlaLysAl aGluAlaAla GlyHisArgA spThrLeuTyr

1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCTGCT GGATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG
     GTGCTACGAC TATTTCACCC AGTTGTTTTG GCCCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTGA ACGGTTCGTC
355   ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln

1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA
     TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTCACAC TAAGAGAAGT CCTTCACTCT
388  LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluGl yAsnAlaAsp SerAlaXaaS erOC*

1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC
     GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG

1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT
     GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTCG ACTTACACTA TTATTCCTGT GATACCTTTA
```

FIG._1B

```
1601 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA TTGTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT
     CAGACCTAGT AAGGCAAACA CGCATGAAAC TCTAAACCAA ACCCTACAGT AACAAAAGTG TCGTGAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA

1701 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAG GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC
     AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTC CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACCGG CGGTACCGG
```

FIG._1C

```
  1 MEQRGQNAPAASGARKRHGPGPREARGARPGLRVPKTLVLVVAAVLLLVSAESALITQQD
 61 LAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCLRCTRCD
121 SGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVH
181 KESGIIIGVTVAAVVLIVAVFVCKSLLWKKVLPYLKGICSGGGGDPERVDRSSQRPGAED
241 NVLNEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEAERSQRRRLLVPA
301 NEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAAGHRDTLYTMLIKW
361 VNKTGRDASVHTLLDALETLGERLAKQKIEDHLLSSGKFMYLEGNADSALS
```

FIG._2A

```
Apo2       F A D L V P F D S W E P L M R K L G L M D N E I K V A K A E A A - - G H R D T L
DR4        F A N I V P F D S W D Q L M R Q L D L T K N E I D V V R A G T A - - G P G D A L
Apo3/DR3   V M D A V P A R R W K E F V R T L G L R E A E I E A V E V E I G R - - F R D Q Q
TNFR1      V V E N V P P L R W K E F V R R L G L S D H E I D R L E L Q N G R - C L R E A Q
Fas/Apo1   I A G V M T L S Q V K G F V R K N G V N E A K I D E I K N D N V Q D T A E Q K V

Apo2       Y T M L I K W V N K T G R D - A S V H T L L D A L E T L G E R L A K Q K I E D
DR4        Y A M L M K W V N K T G R N - A S I H T L L D A L E R M E E R H A K E K I Q D
Apo3/DR3   Y E M L K R W R Q Q Q P - - - A G L G A V Y A A L E R M G L D G C V E D L R S
TNFR1      Y S M L A T W R R R T P R R E A T L E L L G R V L R D M D L L G C L E D I E E
Fas/Apo1   - Q L L R N W H Q L H G K K E A Y - D T L I K D L K K A N L C T L A E K I Q T
```

FIG._2B

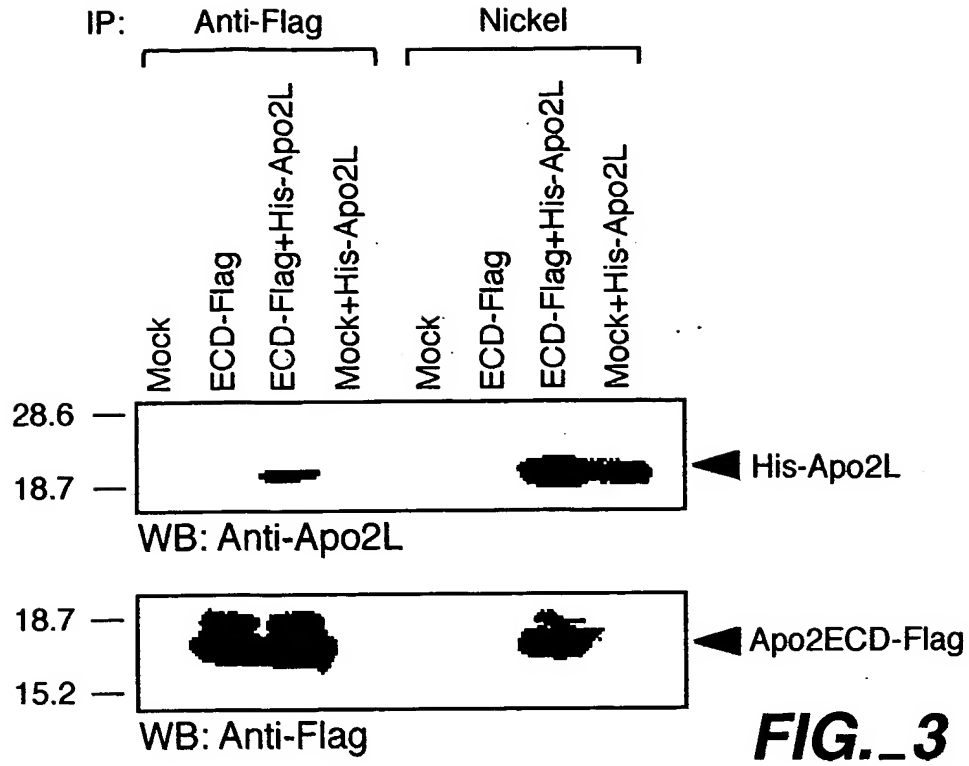


FIG._3

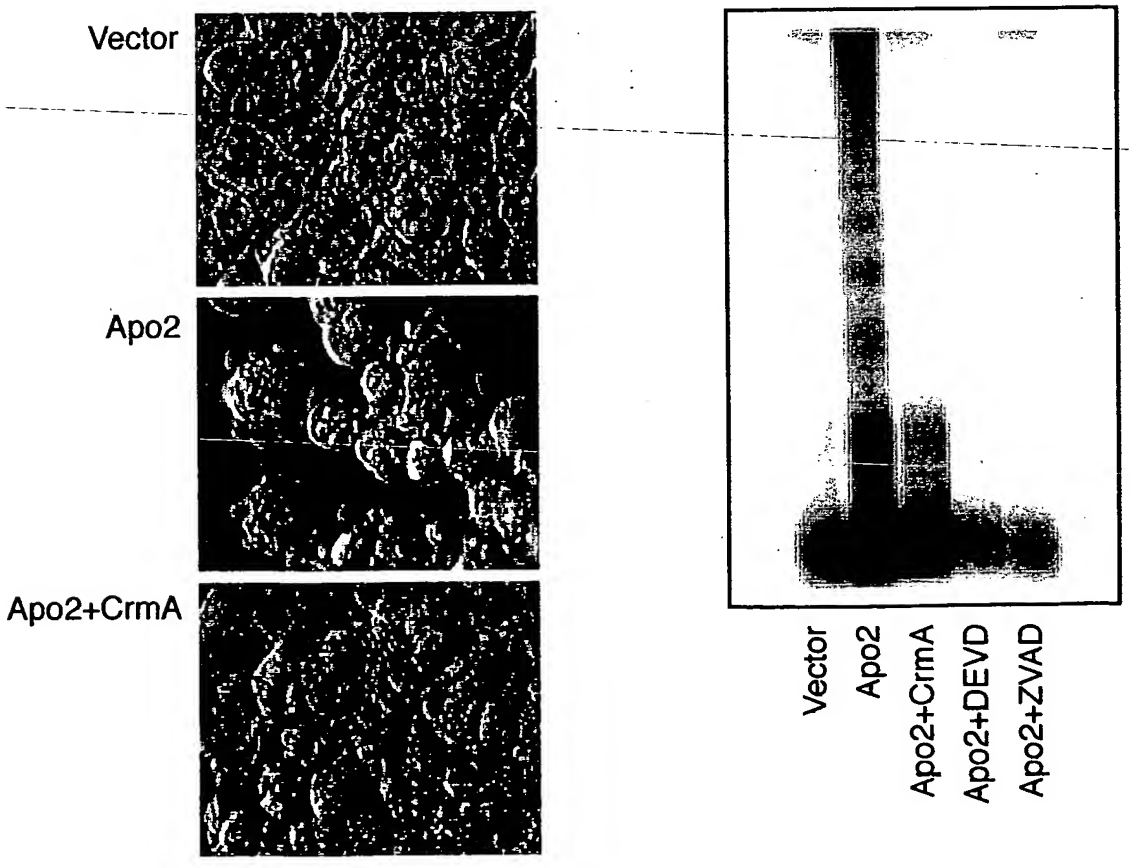


FIG._4A

FIG._4B

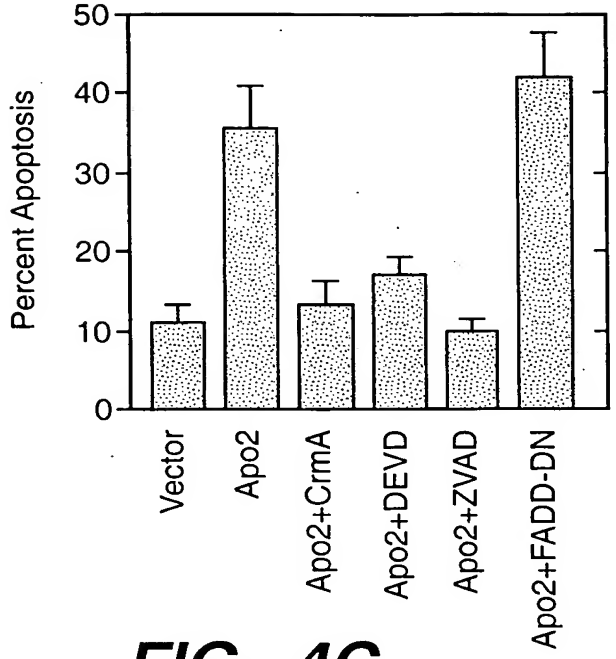


FIG._4C

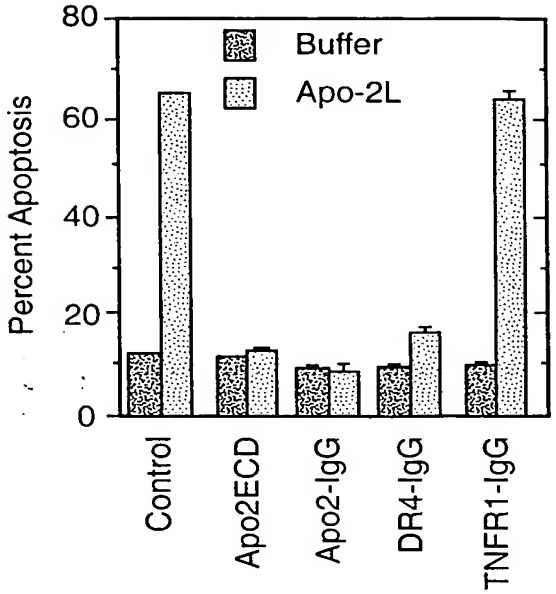


FIG._4D

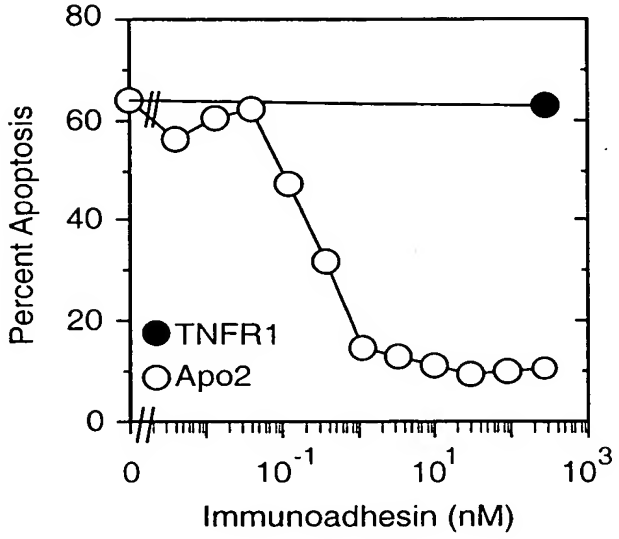


FIG._4E

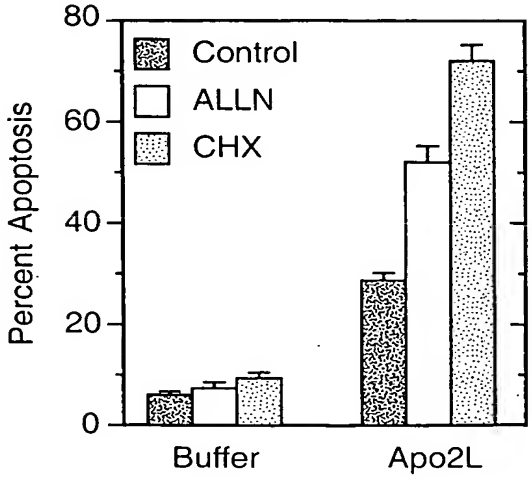


FIG._5C

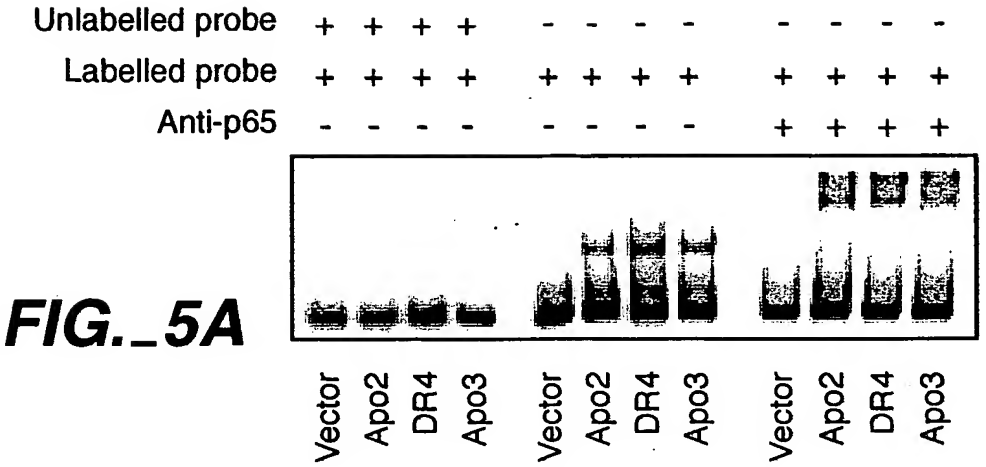


FIG._5A

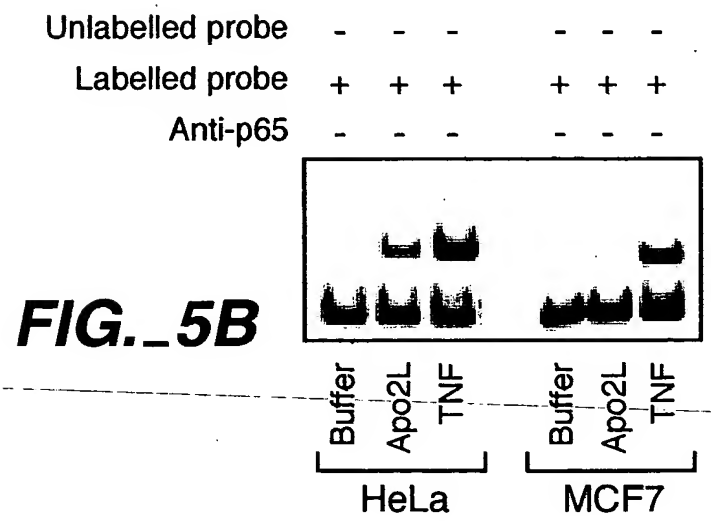


FIG._5B

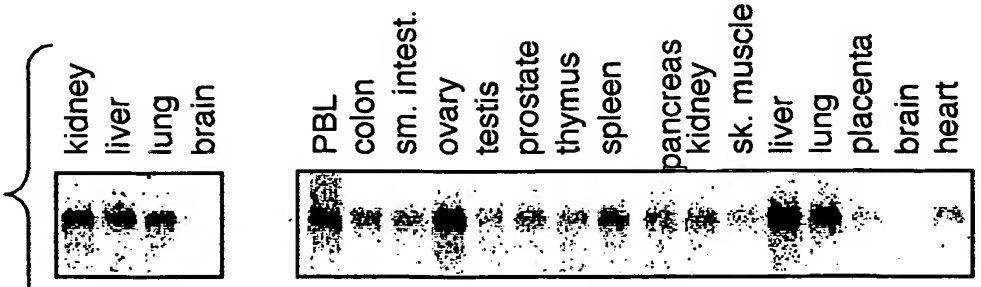


FIG._6A

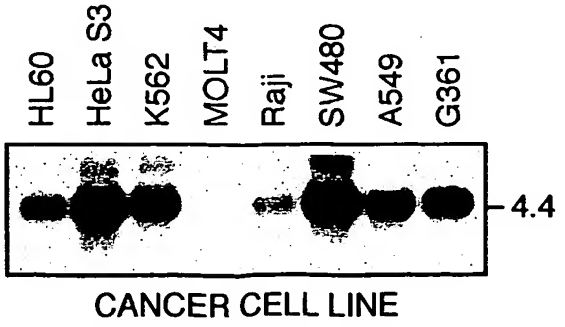


FIG._6B

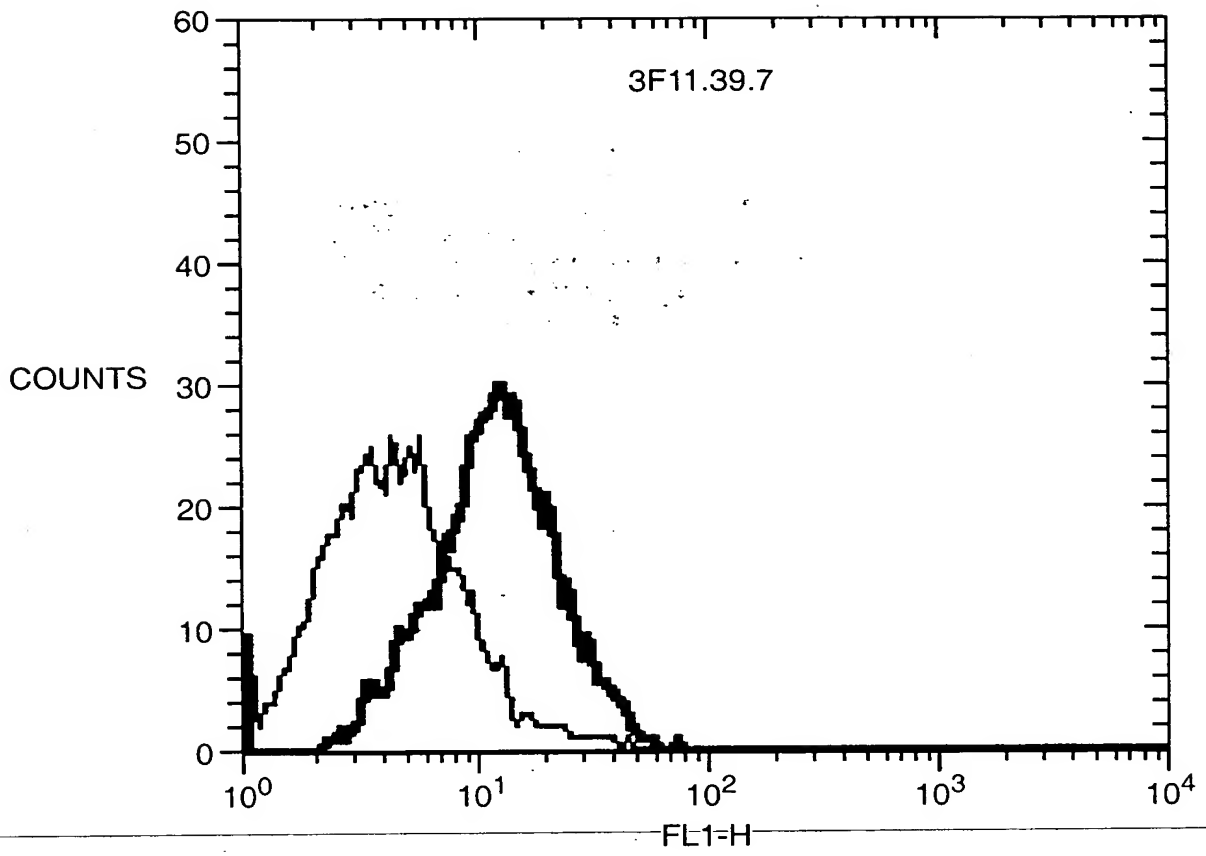


FIG._7

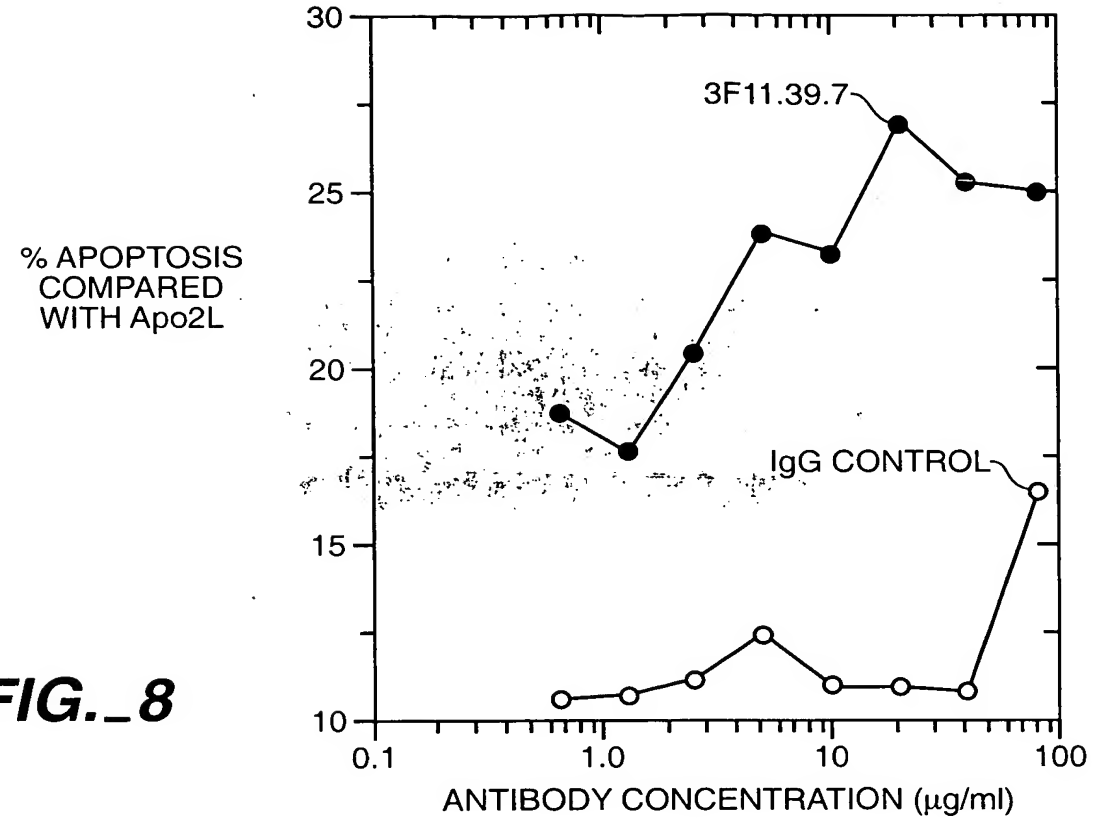

30
25
20
15
10
3F11.39.7
IgG CONTROL
% APOPTOSIS COMPARED WITH Apo2L
0.1
1.0
10
100
ANTIBODY CONCENTRATION (μg/ml)

FIG._8

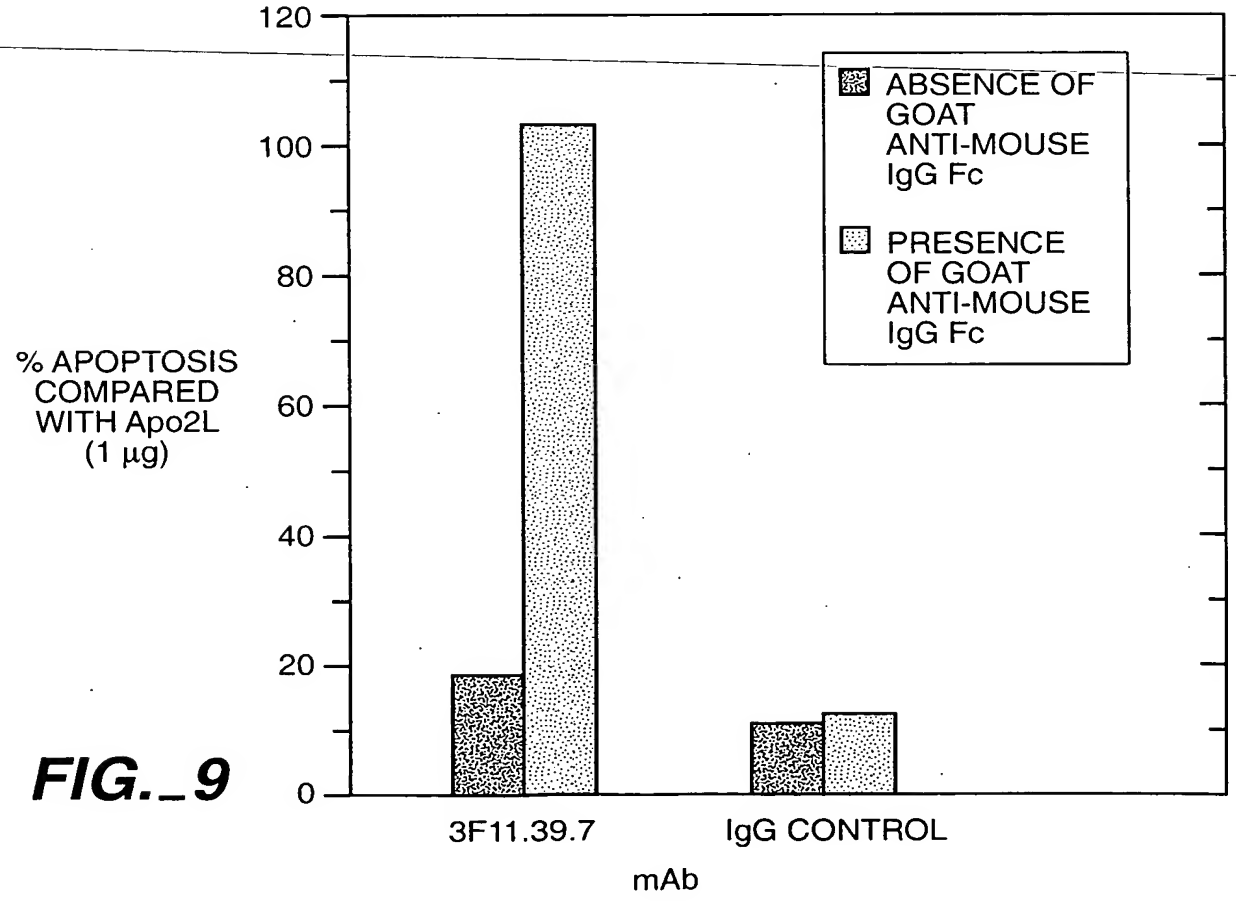

120
100
80
60
40
20
0
% APOPTOSIS COMPARED WITH Apo2L (1 μg)
ABSENCE OF GOAT ANTI-MOUSE IgG Fc
PRESENCE OF GOAT ANTI-MOUSE IgG Fc
3F11.39.7
IgG CONTROL
mAb

FIG._9

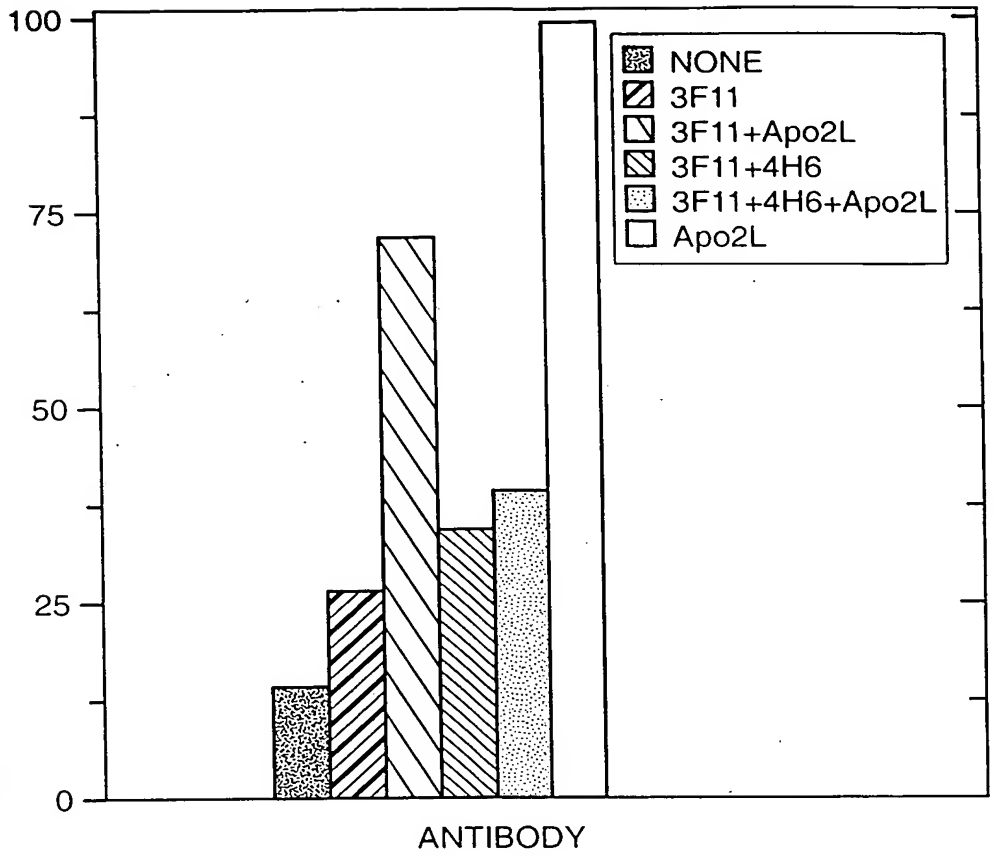

100
75
50
25
0
NONE
3F11
3F11+Apo2L
3F11+4H6
3F11+4H6+Apo2L
Apo2L
% APOPTOSIS
OF 9D CELLS
ANTIBODY

FIG._10

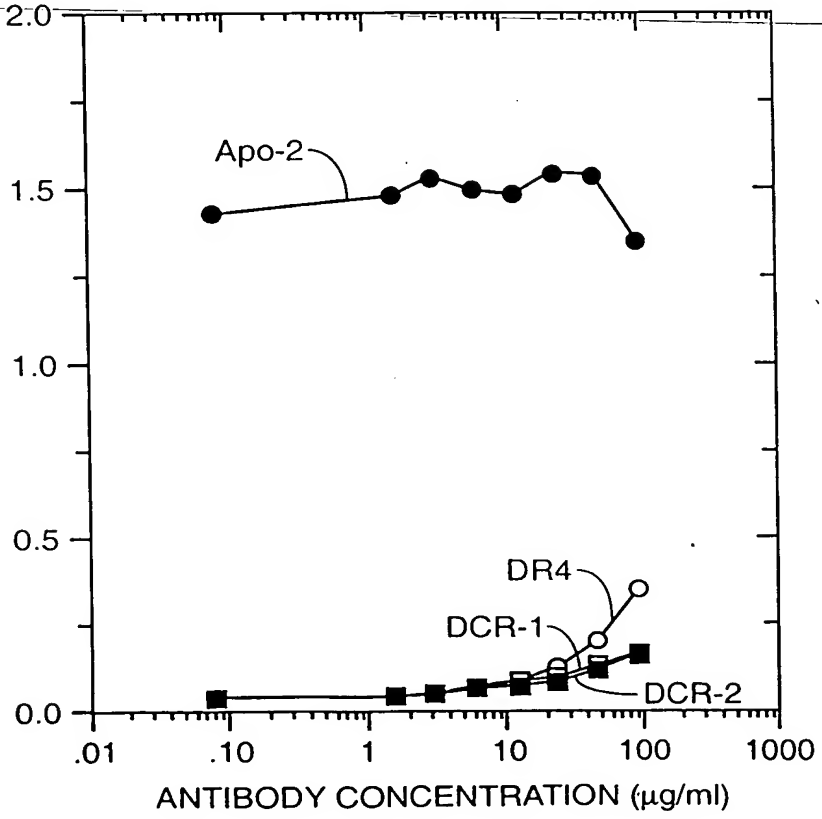

2.0
1.5
1.0
0.5
0.0
Apo-2
DR4
DCR-1
DCR-2
OD 450/620
.01
.10
1
10
100
1000
ANTIBODY CONCENTRATION (µg/ml)

FIG._11

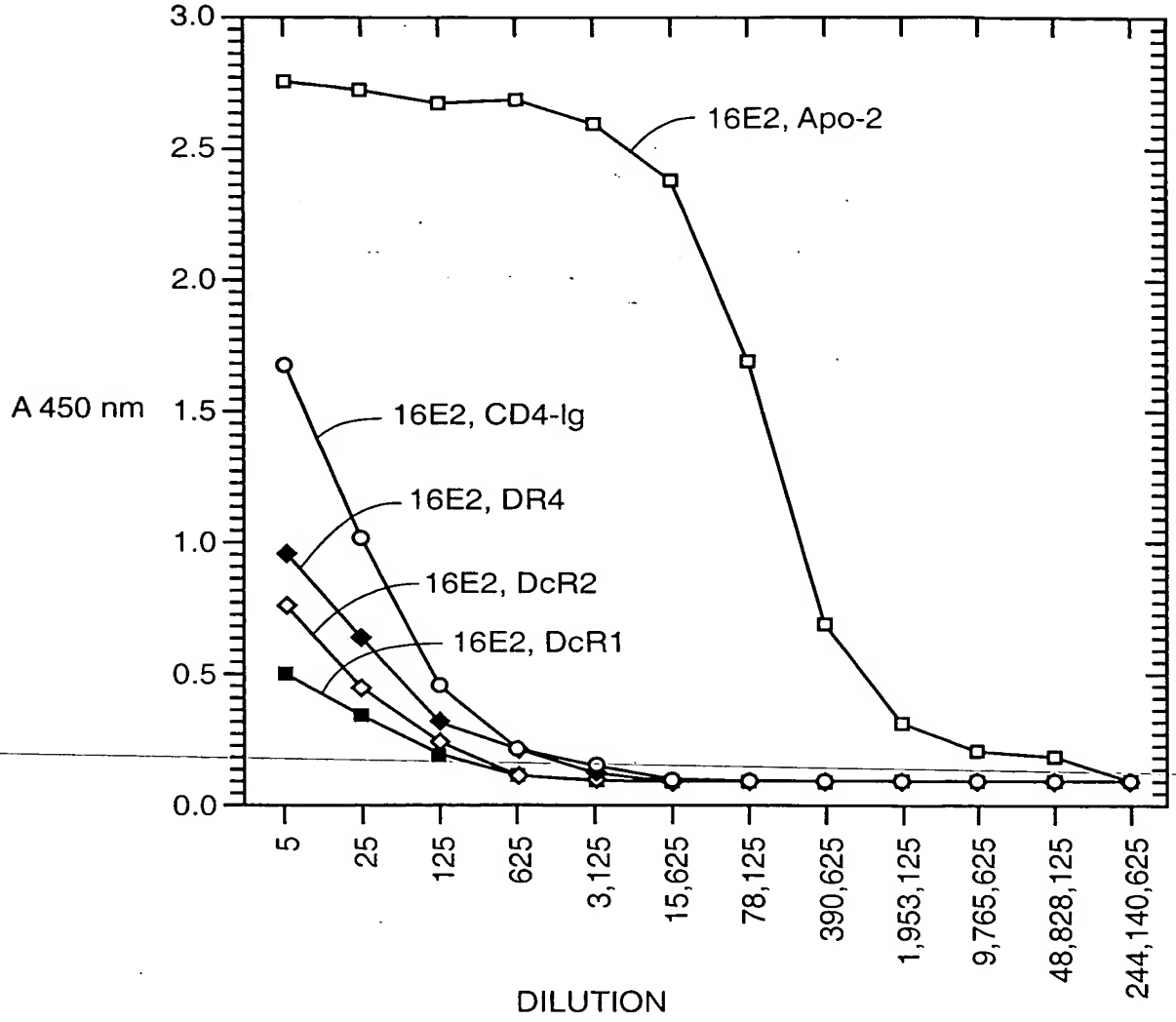

3.0
2.5
2.0
1.5
1.0
0.5
0.0
A 450 nm
16E2, Apo-2
16E2, CD4-Ig
16E2, DR4
16E2, DcR2
16E2, DcR1
5
25
125
625
3,125
15,625
78,125
390,625
1,953,125
9,765,625
48,828,125
244,140,625
DILUTION

FIG._12A

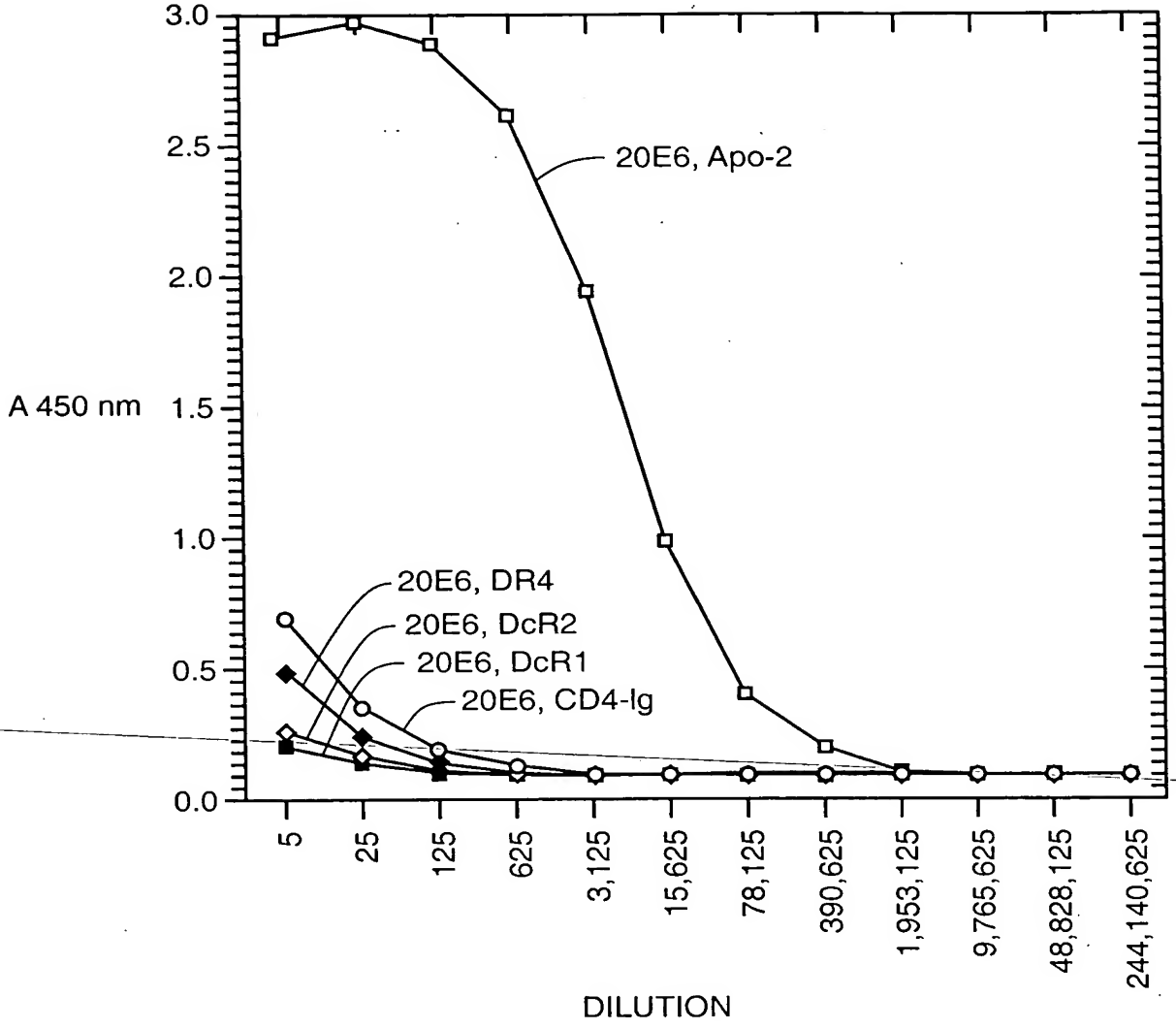

3.0
2.5
2.0
1.5
1.0
0.5
0.0
A 450 nm
20E6, Apo-2
20E6, DR4
20E6, DcR2
20E6, DcR1
20E6, CD4-Ig
5
25
125
625
3,125
15,625
78,125
390,625
1,953,125
9,765,625
48,828,125
244,140,625
DILUTION

FIG._12B

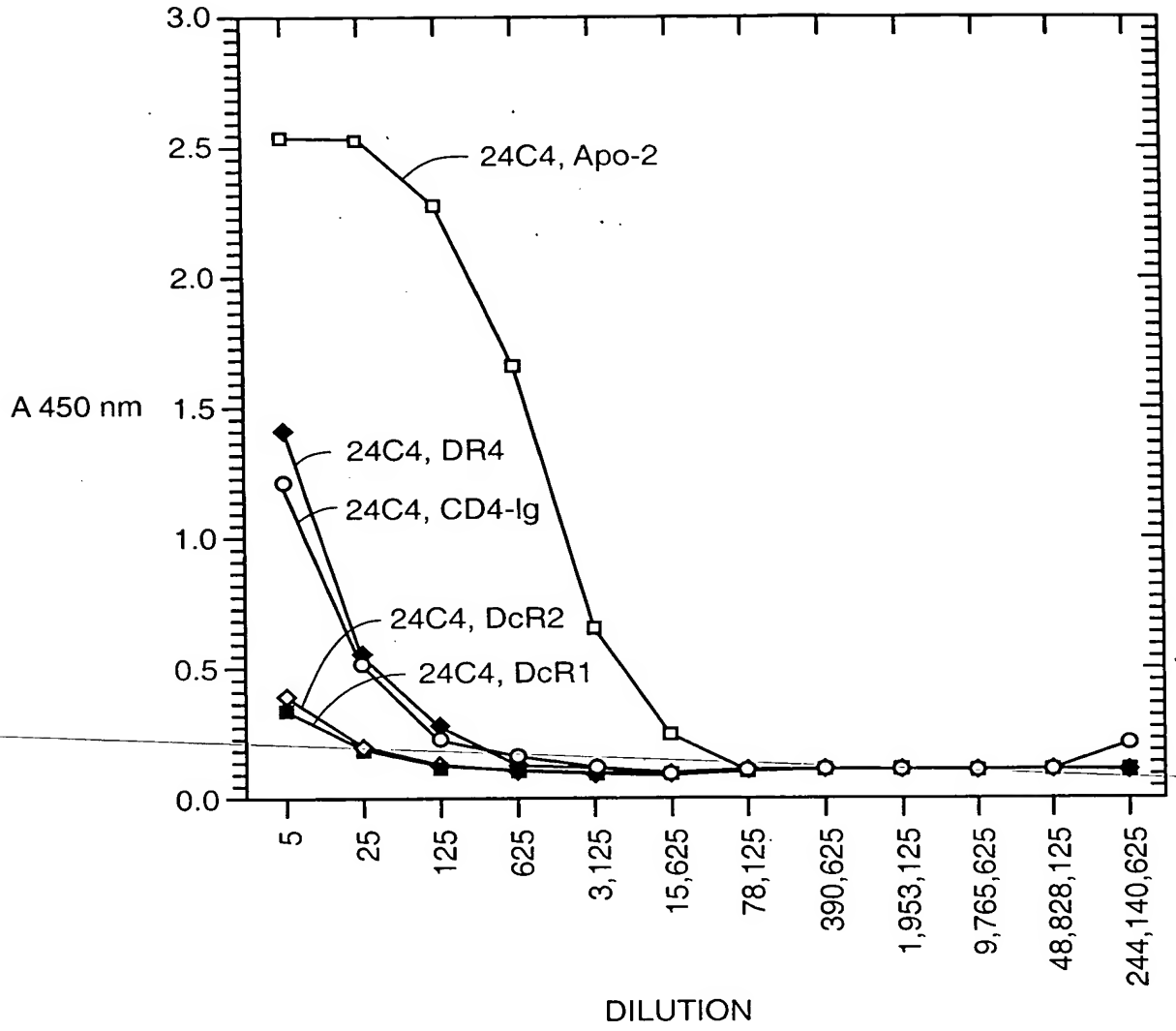
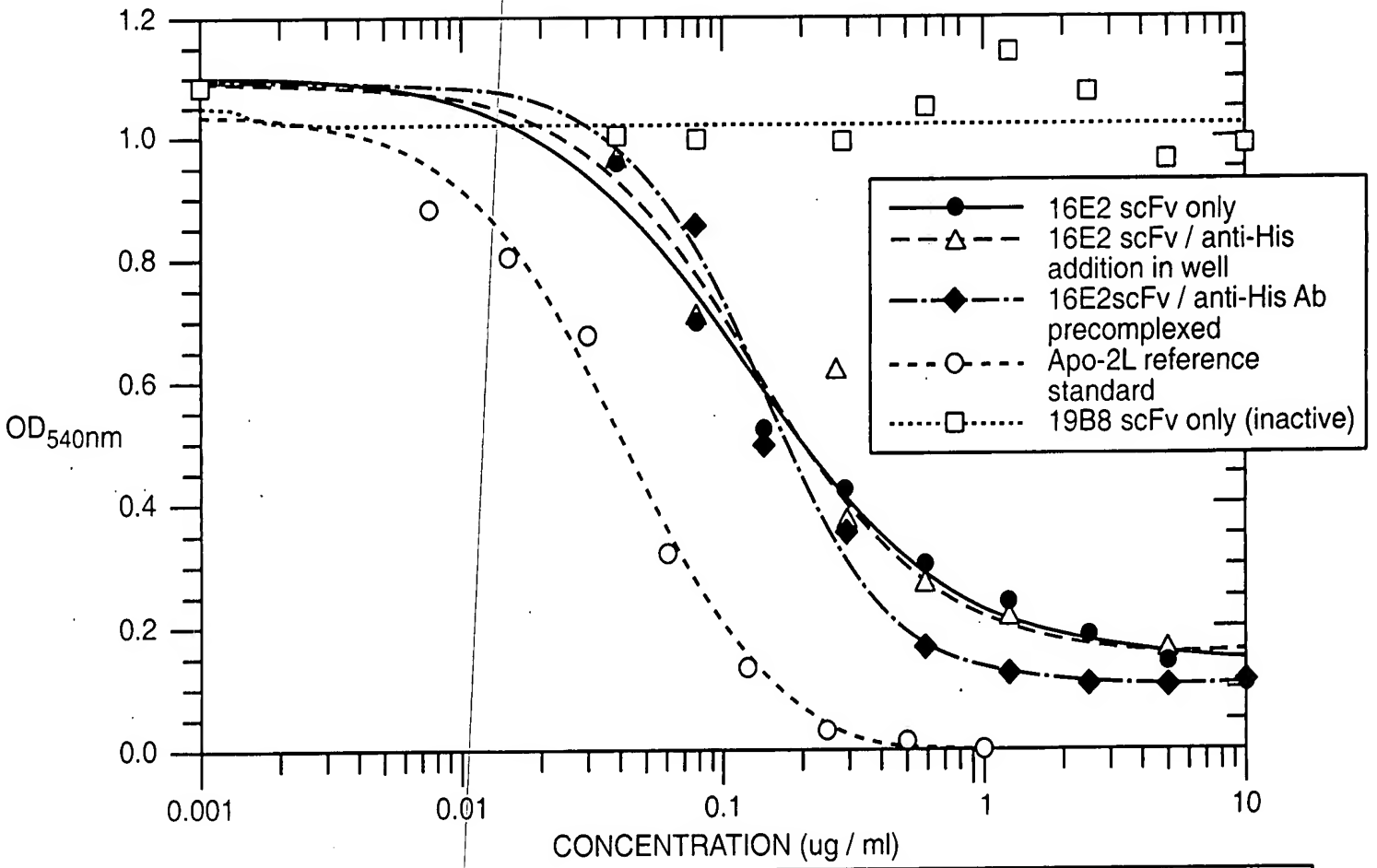

3.0
2.5
2.0
1.5
1.0
0.5
0.0
A 450 nm
24C4, Apo-2
24C4, DR4
24C4, CD4-Ig
24C4, DcR2
24C4, DcR1
5
25
125
625
3,125
15,625
78,125
390,625
1,953,125
9,765,625
48,828,125
244,140,625
DILUTION

FIG._12C

FIG._13A



Apo-2L REFERENCE STANDARD		
	VALUE	ERROR
m1	1.0383	0.048755
m2	1.4661	0.25023
m3	**0.040308**	**0.0052093**
m4	-0.023006	0.040857
Chisq	0.013011	NA
R	0.99551	NA

16E2 scFv ONLY		
	VALUE	ERROR
m1	1.105	0.045677
m2	1.1094	0.1698
m3	**0.12447**	**0.018661**
m4	0.13897	0.031341
Chisq	0.011781	NA
R	0.99448	NA

FIG._13B

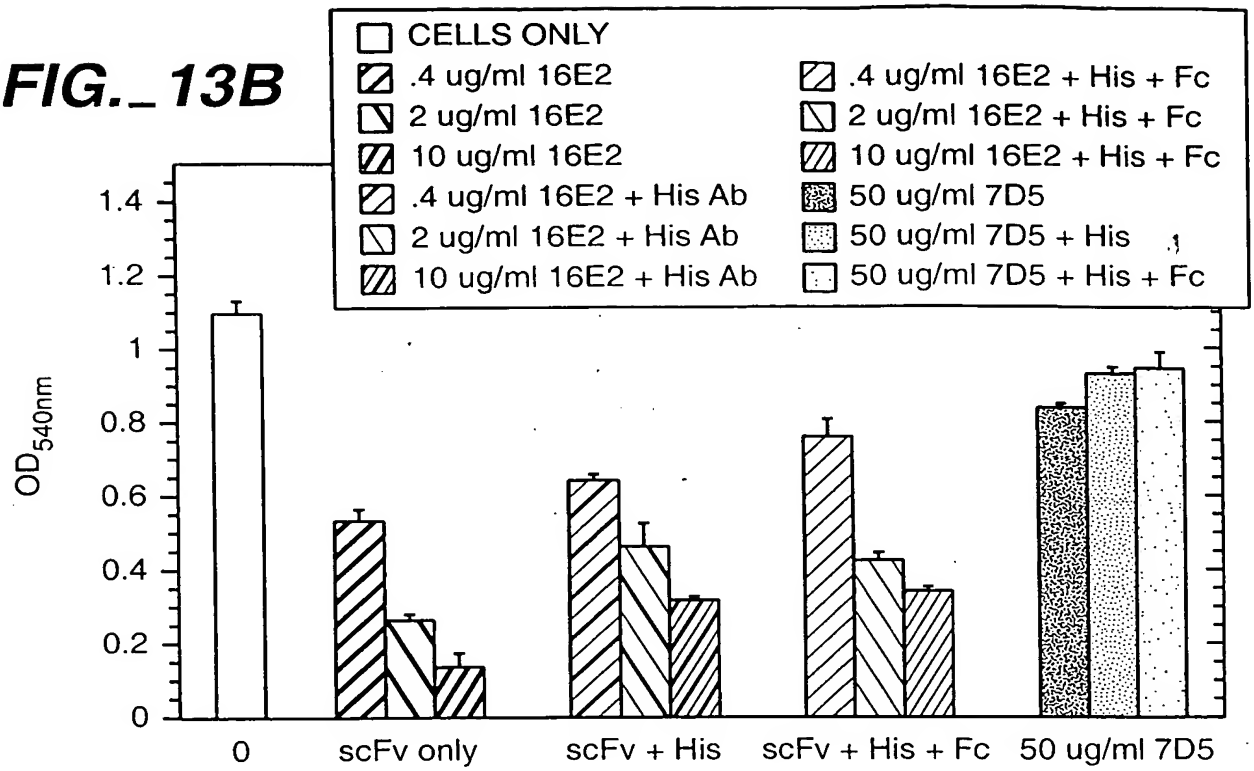


FIG._13C

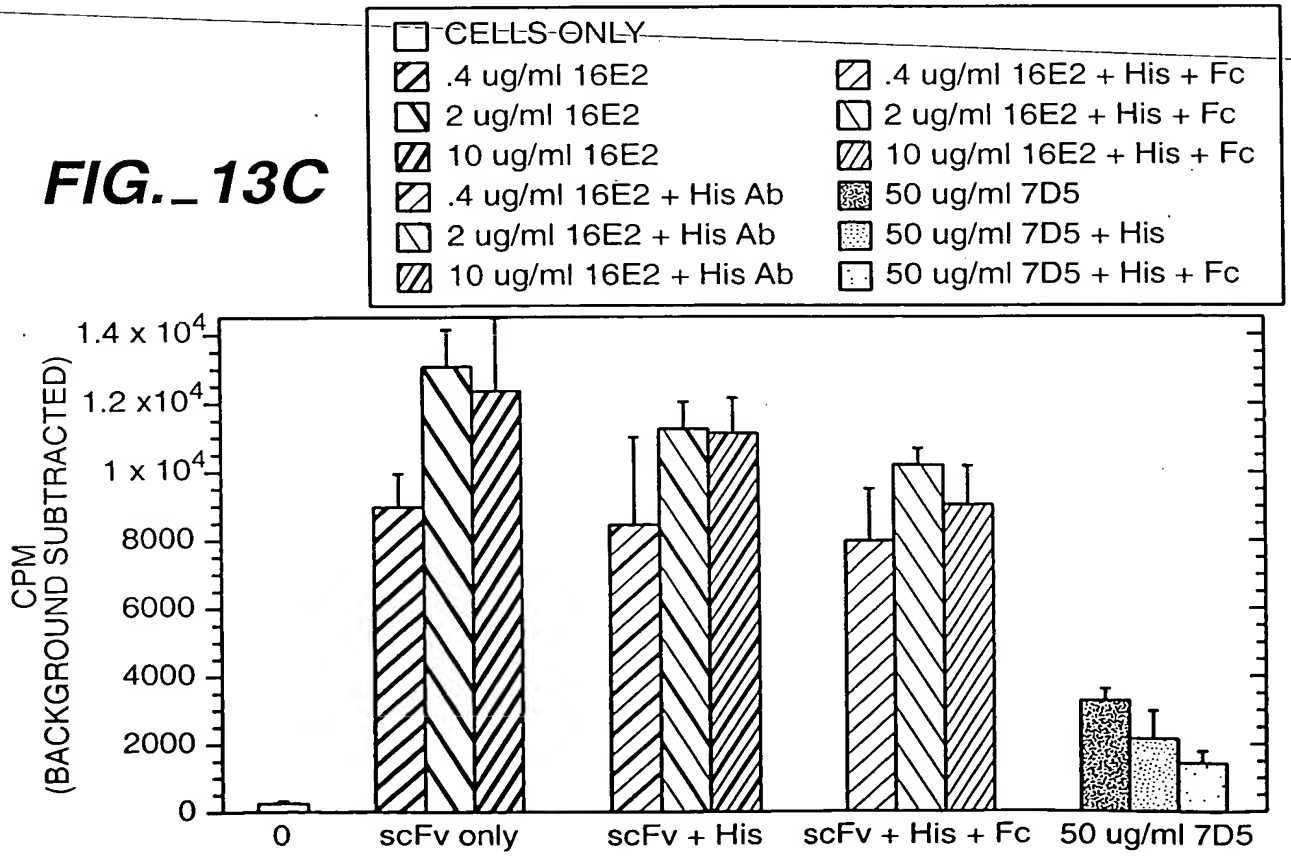
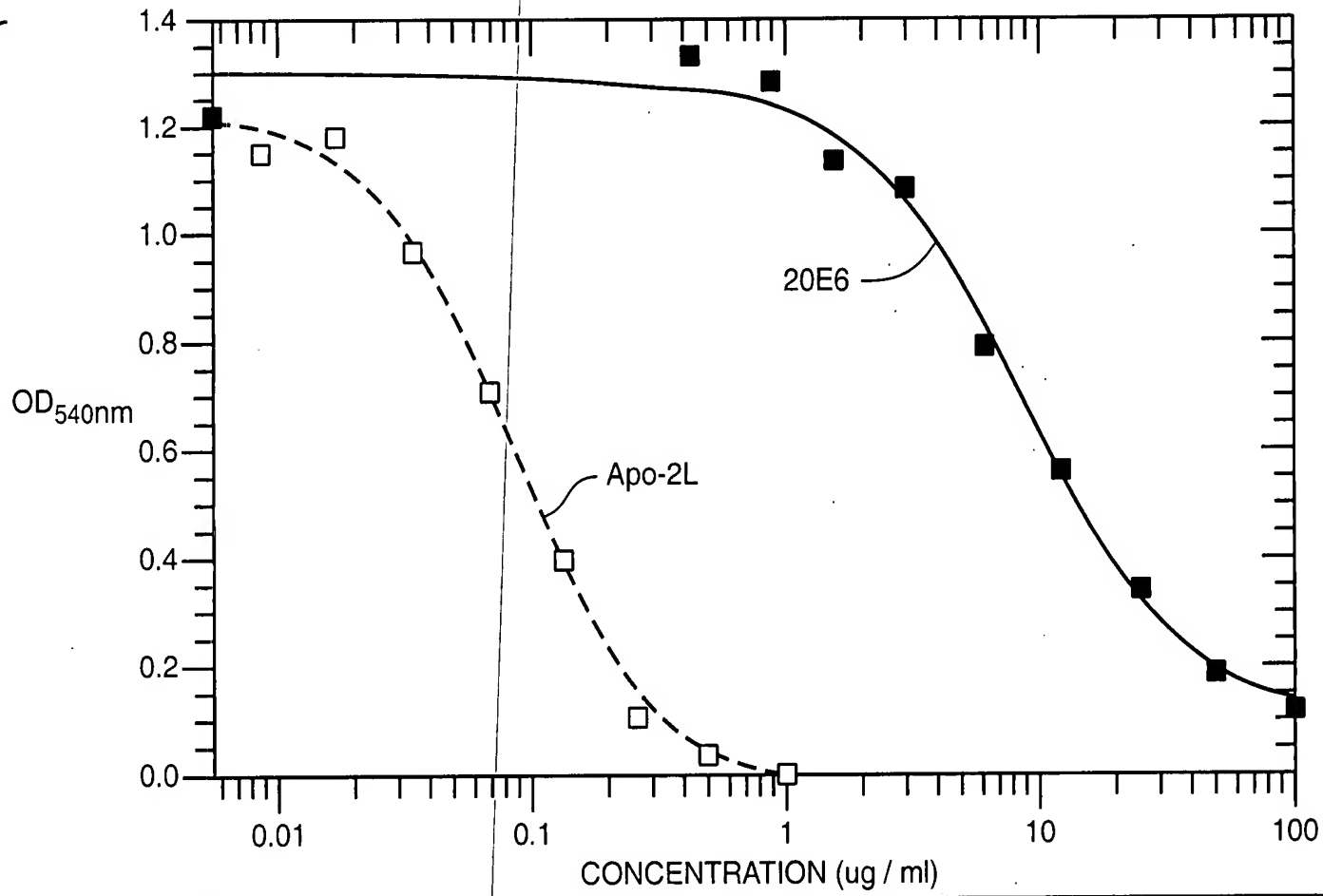


FIG._14A



Apo-2L		
	VALUE	ERROR
m1	1.2216	0.028142
m2	1.6356	0.17759
m3	**0.0780**	**0.00529**
m4	-0.025859	0.033322
Chisq	0.0058166	NA
R	0.99864	NA

scFv 20E6		
	VALUE	ERROR
m1	1.2948	0.038022
m2	1.3318	0.22832
m3	**8.6124**	**1.2249**
m4	0.077139	0.068356
Chisq	0.017679	NA
R	0.99565	NA

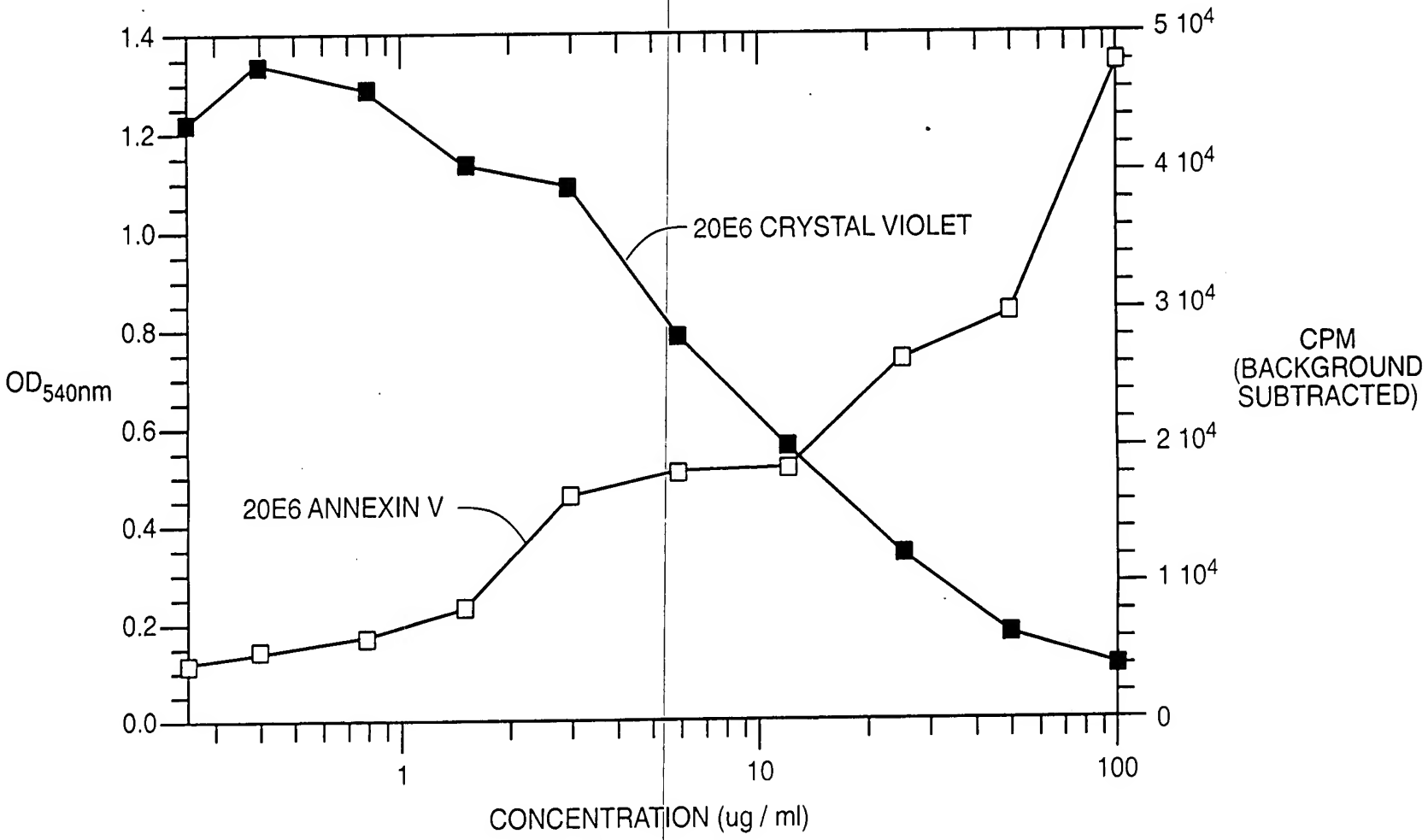
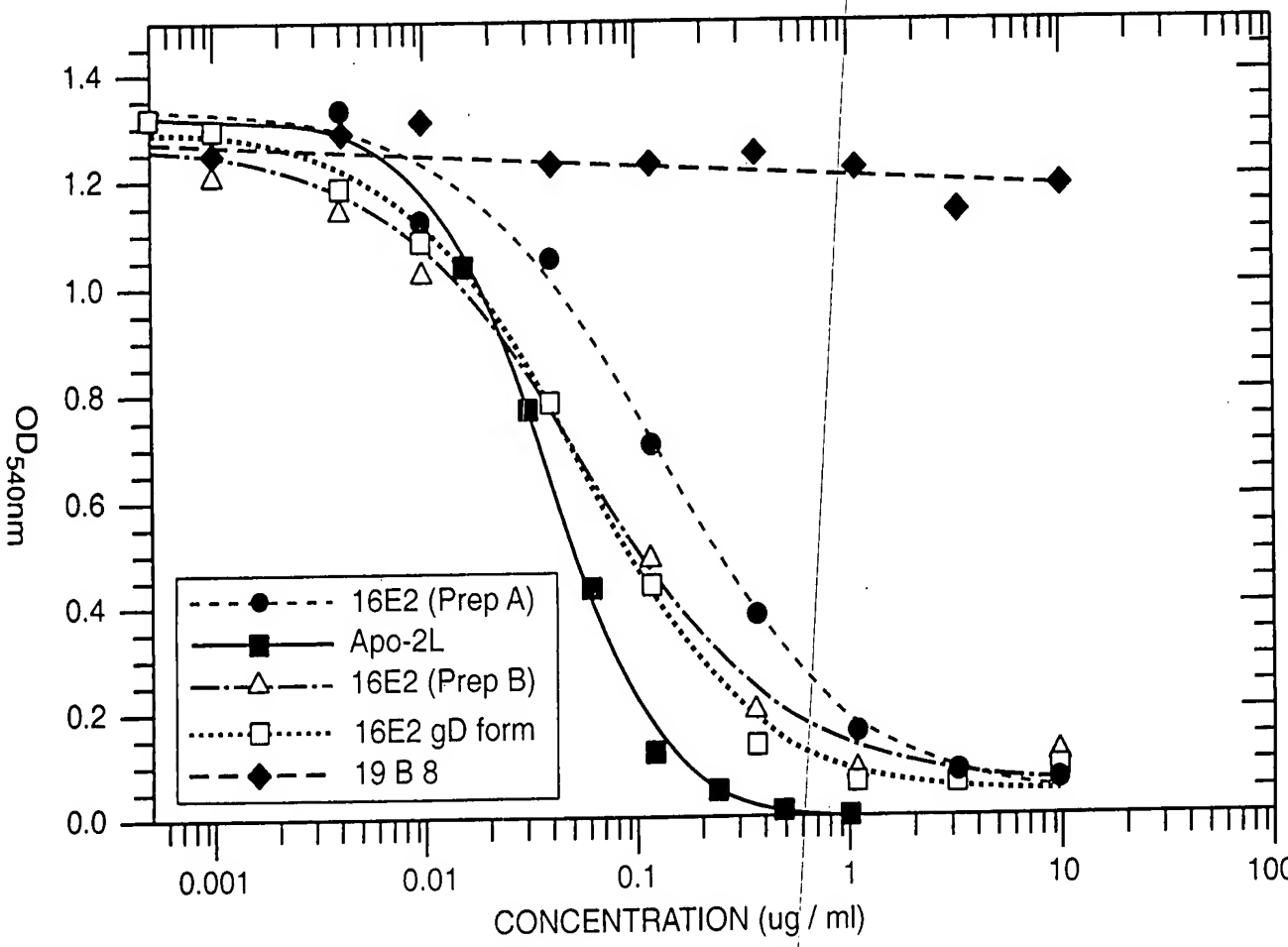


FIG._14B



16E2 gD form		
	VALUE	ERROR
m1	1.2927	0.031233
m2	1.0515	0.12327
m3	**0.0529**	**0.00630**
m4	0.038924	0.028704
Chisq	0.0099802	NA
R	0.99812	NA

Apo-2L STANDARD		
	VALUE	ERROR
m1	1.3125	0.025484
m2	1.5904	0.1161
m3	**0.0384**	**0.00201**
m4	-0.018045	0.020658
Chisq	0.0039739	NA
R	0.99916	NA

16E2 (Prep B)		
	VALUE	ERROR
m1	1.2703	0.039588
m2	0.90584	0.12741
m3	**0.0565**	**0.00904**
m4	0.053232	0.037078
Chisq	0.012564	NA
R	0.99728	NA

FIG._14C

```
ATGACCATGA TTACGCCAAG CTTTGGAGCC TTTTTTTTGG AGATTTTCAA 50
CGTGAAAAAA TTATTATTCG CAATTCCTTT AGTTGTTCCT TTCTATGCGG 100
CCCAGCCGGC CATGGCCGAG GTGCAGCTGG TGCAGTCTGG GGGAGGTGTG 150
GAACGGCCGG GGGGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGATTCAC 200
CTTTGATGAT TATGGCATGA GCTGGGTCCG CCAAGCTCCA GGGAAGGGGC 250
TGGAGTGGGT CTCTGGTATT AATTGGAATG GTGGTAGCAC AGGATATGCA 300
GACTCTGTGA AGGGCCGAGT CACCATCTCC AGAGACAACG CCAAGAACTC 350
CCTGTATCTG CAAATGAACA GCCTGAGAGC CGAGGACACG GCCGTATATT 400
ACTGTGCGAA AATCCTGGGT GCCGGACGGG GCTGGTACTT CGATCTCTGG 450
GGGAAGGGGA CCACGGTCAC CGTCTCGAGT GGTGGAGGCG GTTCAGGCGG 500
AGGTGGCAGC GGCGGTGGCG GATCGTCTGA GCTGACTCAG GACCCTGCTG 550
TGTCTGTGGC CTTGGGACAG ACAGTCAGGA TCACATGCCA AGGAGACAGC 600
CTCAGAAGCT ATTATGCAAG CTGGTACCAG CAGAAGCCAG GACAGGCCCC 650
TGTACTTGTC ATCTATGGTA AAAACAACCG GCCCTCAGGG ATCCCAGACC 700
GATTCTCTGG CTCCAGCTCA GGAAACACAG CTTCCTTGAC CATCACTGGG 750
GCTCAGGCGG AAGATGAGGC TGACTATTAC TGTAACTCCC GGGACAGCAG 800
TGGTAACCAT GTGGTATTCG GCGGAGGGAC CAAGCTGACC GTCCTAGGTG 850
CGGCCGCACA TCATCATCAC CATCACGGGG CCGCAGAACA AAAACTCATC 900
TCAGAAGAGG ATCTGAATGG GGCCGCATAG 930
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FIG._15A

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ATGACCATGA TTACGCCAAG CTTTGGAGCC TTTTTTTTGG AGATTTTCAA 50
CGTGAAAAAA TTATTATTCG CAATTCCTTT AGTTGTTCCT TTCTATGCGG 100
CCCAGCCGGC CATGGCCGGG GTGCAGCTGG TGGAGTCTGG GGGAGGCTTG 150
GTCCAGCCTG GGGGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGATTCAC 200
CTTTAGTAGC TATTGGATGA GCTGGGTCCG CCAGGCTCCA GGGAAGGGGC 250
TGGAGTGGGT GGCCAACATA AAGCAAGATG GAAGTGAGAA ATACTATGTG 300
GACTCTGTGA AGGGCCGATT CACCATCTCC AGAGACAACG CCAAGAACTC 350
ACTGTATCTG CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT 400
ACTGTGCGAG AGATCTTTTA AAGGTCAAGG GCAGCTCGTC TGGGTGGTTC 450
GACCCCTGGG GGAGAGGGAC CACGGTCACC GTCTCGAGTG GTGGAGGCGG 500
TTCAGGCGGA GGTGGTAGCG GCGGTGGCGG ATCGTCTGAG CTGACTCAGG 550
ACCCTGCTGT GTCTGTGGCC TTGGGACAGA CAGTCAGGAT CACATGCCAA 600
GGAGACAGCC TCAGAAGCTA TTATGCAAGC TGGTACCAGC AGAAGCCAGG 650
ACAGGCCCCT GTACTTGTCA TCTATGGTAA AAACAACCGG CCCTCAGGGA 700
TCCCAGACCG ATTCTCTGGC TCCAGCTCAG GAAACACAGC TTCCTTGACC 750
ATCACTGGGG CTCAGGCGGA AGATGAGGCT GACTATTACT GTAACTCCCG 800
GGACAGCAGT GGTAACCATG TGGTATTCGG CGGAGGGACC AAGCTGACCG 850
TCCTAGGTGC GGCCGCACAT CATCATCACC ATCACGGGGC CGCAGAACAA 900
AAACTCATCT CAGAAGAGGA TCTGAATGGG GCCGCATAG 939
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FIG._15B

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ATGACCATGA TTACGCCAAG CTTTGGAGCC TTTTTTTTGG AGATTTTCAA 50
CGTGAAAAAA TTATTATTCG CAATTCCTTT AGTTGTTCCT TTCTATGCGG 100
CCCAGCCGGC CATGGCCCAG GTGCAGCTGG TGCAGTCTGG GGGAGGCGTG 150
GTCCAGCCTG GGCGGTCCCT GAGACTCTCC TGTGCAGCTT CTGGGTTCAT 200
TTTCAGTAGT TATGGGATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC 250
TGGAGTGGGT GGCAGGTATT TTTTATGATG GAGGTAATAA ATACTATGCA 300
GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC 350
GCTGTATCTG CAAATGAACA GCCTGAGAGC TGAGGACACG GCTGTGTATT 400
ACTGTGCGAG AGATAGGGGC TACTACTACA TGGACGTCTG GGGCAAAGGG 450
ACCACGGTCA CCGTCTCCTC AGGTGGAGGC GGTTCAGGCG GAGGTGGCTC 500
TGGCGGTGGC GGATCGCAGT CTGTGTTGAC GCAGCCGCCC TCAGTGTCTG 550
GGGCCCCAGG ACAGAGGGTC ACCATCTCCT GCACTGGGAG AAGCTCCAAC 600
ATCGGGGCAG GTCATGATGT ACACTGGTAC CAGCAACTTC CAGGAACAGC 650
CCCCAAACTC CTCATCTATG ATGACAGCAA TCGGCCCTCA GGGGTCCCTG 700
ACCGATTCTC TGGCTCCAGG TCTGGCACCT CAGCCTCCCT GGCCATCACT 750
GGGCTCCAGG CTGAAGATGA GGCTGATTAT TACTGCCAGT CCTATGACAG 800
CAGCCTGAGG GGTTCGGTAT TCGGCGGAGG GACCAAGGTC ACTGTCCTAG 850
GTGCGGCCGC ACATCATCAT CACCATCACG GGGCCGCAGA ACAAAAACTC 900
ATCTCAGAAG AGGATCTGAA TGGGGCCGCA TAG 933
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FIG._15C

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                      signal                                      Heavy chain
Apo-2.16E2.his     1 MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAEVQLVQSGGGV
Apo-2.20E6.his     1 MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGL
Apo-2.24C4.his     1 MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAQVQLVQSGGGV

                                       CDR1               CDR2
Apo-2.16E2.his    51 ERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGYA
Apo-2.20E6.his    51 VQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV
Apo-2.24C4.his    51 VQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYA

                                                          CDR3
Apo-2.16E2.his   101 DSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKIL----GAGRGWY
Apo-2.20E6.his   101 DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGW-
Apo-2.24C4.his   101 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD--------RGYY

                                                   Light chain
Apo-2.16E2.his   147 F-DLWGKGTTVTVSSGGGGSGGGGSGGGGS-SELTQDPAVSVALGQTVRI
Apo-2.20E6.his   150 F-DPWGRGTTVTVSSGGGGSGGGGSGGGGS-SELTQDPAVSVALGQTVRI
Apo-2.24C4.his   143 YMDVWGKGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTI

                       CDR1                        CDR2
Apo-2.16E2.his   195 TCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSG
Apo-2.20E6.his   198 TCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSG
Apo-2.24C4.his   193 SCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSRSG

                                         CDR3
Apo-2.16E2.his   242 NTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHH
Apo-2.20E6.his   245 NTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHH
Apo-2.24C4.his   243 TSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHH

Apo-2.16E2.his   292 HGAAEQKLISEEDLNGAA
Apo-2.20E6.his   295 HGAAEQKLISEEDLNGAA
Apo-2.24C4.his   293 HGAAEQKLISEEDLNGAA
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FIG._16